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Scientific and Technical Information Center

SEARCH REQUEST FORM

Requester's Full Name: Jeffrey E. Russell Examiner #: 62785 Date: 6-17-2005  
Art Unit: 1654 Phone Number: 2-0969 Serial Number: 10/666,095  
Location (Bldg/Room#): REM 3 D17 (Mailbox #): 3C18 Results Format Preferred (circle): PAPER (DISK)  
\*\*\*\*\*

To ensure an efficient and quality search, please attach a copy of the cover sheet, claims, and abstract or fill out the following:

Title of Invention: Anti-fibril Peptides  
Inventors (please provide full names): R. Hammer, Y. Fu, J. Aucoin, T. Miller, M. McLoughlin,  
R. McCerley  
Earliest Priority Date: 9-18-2003

Search Topic:

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc., if known.

\*For Sequence Searches Only\* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

Please search SEQ TO NO: 7 (KX VXF) in the U.S. patent application sequence database (primarily published, issued), ~~and~~ and in the Uniprot/PIR/Genbank. Please require any hits to have 30 or fewer residues.

Thank you.  
JER

STAFF USE ONLY

Type of Search

Vendors and cost where applicable

Searcher: _____	_____ NA Sequence (#)	_____ STN	_____ Dialog
Searcher Phone #: _____	_____ AA Sequence (#)	_____ Questel/Orbit	_____ Lexis/Nexis
Searcher Location: _____	_____ Structure (#)	_____ Westlaw	_____ WWW/Internet
Date Searcher Picked Up: _____	_____ Bibliographic	_____ In-house sequence systems	
Date Completed: _____	_____ Litigation	_____ Commercial	_____ Oligomer
Searcher Prep & Review Time: _____	_____ Fulltext	_____ Interference	_____ SPDI
Online Time: _____	_____ Other	_____ Other (specify)	

OM protein - protein search, using sw model

Run on: June 29, 2005, 15:22:51 ; Search time 160 Seconds  
(without alignments)  
14.504 Million cell updates/sec

Title: US-10-666-095-7  
Perfect score: 18  
Sequence: 1 KXVFX 6

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 811763

Minimum DB seq length: 0  
Maximum DB seq length: 30

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	% Query		Length	DB	ID	Description
	Score	Match				
1	15	83.3	9	4	AAM24833	Aam24833 Human MHC
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7	15	83.3	10	4	AAM24793	Aam24793 Human MHC
8	15	83.3	10	4	AAM24913	Aam24913 Human MHC
9	15	83.3	10	4	AAM24898	Aam24898 Human MHC

10	15	83.3	11	2	AAW23266	Aaw23266	Tumour ne
11	15	83.3	11	4	AAB72856	Aab72856	Human p53
12	15	83.3	13	8	ADH89766	Adh89766	Cell pene
13	15	83.3	14	3	AAV56963	Aay56963	Constitut
14	15	83.3	15	2	AAV52094	Aay52094	HIV-1 pep
15	15	83.3	15	3	AAV99252	Aay99252	HLA class
16	15	83.3	17	7	ADH48641	Adh48641	Serine hy
17	15	83.3	28	8	ADO81263	Ado81263	Protein s
18	14	77.8	5	2	AAW02330	Aaw02330	Beta-amyl
19	14	77.8	5	2	AAW45963	Aaw45963	Peptide d
20	14	77.8	5	2	AAW45965	Aaw45965	Peptide d
21	14	77.8	5	2	AAW89387	Aaw89387	Beta-amyl
22	14	77.8	5	5	ABG71030	Abg71030	Long form
23	14	77.8	5	5	ABB05176	Abb05176	Beta amyl
24	14	77.8	5	5	ABB05185	Abb05185	Beta amyl
25	14	77.8	5	8	ADJ64081	Adj64081	Human bet
26	14	77.8	5	8	ADJ64090	Adj64090	Human bet
27	14	77.8	5	8	ADQ37367	Adq37367	Beta-amyl
28	14	77.8	6	4	AAB48480	Aab48480	Antifibri
29	14	77.8	6	4	AAB48488	Aab48488	Antifibri
30	14	77.8	6	4	AAB82636	Aab82636	All-D pep
31	14	77.8	6	4	AAB82628	Aab82628	All-D pep
32	14	77.8	6	5	AAU96824	Aau96824	Amyloid t
33	14	77.8	6	5	AAU96816	Aau96816	Amyloid t
34	14	77.8	6	5	AAU11662	Aau11662	Peptide #
35	14	77.8	6	5	AAU11654	Aau11654	Peptide #
36	14	77.8	6	6	AAE35450	Aae35450	Abeta pep
37	14	77.8	6	6	AAE35443	Aae35443	Abeta pep
38	14	77.8	6	8	ADQ37275	Adq37275	Vaccine a
39	14	77.8	6	8	ADQ37267	Adq37267	Vaccine a
40	14	77.8	6	8	ADQ37319	Adq37319	Antifibri
41	14	77.8	6	8	ADQ37327	Adq37327	Antifibri
42	14	77.8	8	2	AAR36140	Aar36140	Hepatitis
43	14	77.8	8	2	AAR84489	Aar84489	Hepatitis
44	14	77.8	8	2	AAR84460	Aar84460	Hepatitis
45	14	77.8	8	4	ABR52221	Abr52221	Mutant Pe

#### ALIGNMENTS

RESULT 1

AAM24833

ID AAM24833 standard; peptide; 9 AA.

XX

AC AAM24833;

XX

DT 04-DEC-2001 (first entry)

XX

DE Human MHC molecule HLA-A11 binding 83P5G4 peptide #10.

XX

KW 83P5G4-related protein; prostate; testis; tissue; cancer; bladder; liver;

KW tumour; kidney; brain; bone; ovary; breast; pancreas; colon; lung; serum;

KW cytostatic; gene therapy; antibody therapy; ribozyme; blood; cervix;

KW single chain monoclonal antibody; urine; uterus; rectum; stomach; human;

KW chromosome 1q31-q32.

XX

OS Homo sapiens.  
 XX  
 PN WO200159115-A2.  
 XX  
 PD 16-AUG-2001.  
 XX  
 PF 09-FEB-2001; 2001WO-US004426.  
 XX  
 PR 09-FEB-2000; 2000US-0181261P.  
 XX  
 PA (UROG-) UROGENESYS INC.  
 XX  
 PI Hubert RS, Afar DEH, Challita-Eid PM, Faris M, Levin E;  
 PI Mitchell SC, Jakobovits A;  
 XX  
 DR WPI; 2001-514669/56.  
 XX  
 PT An isolated 83P5G4-related protein useful as a diagnostic and/or  
 PT therapeutic agent in multiple cancers such as prostate, bladder and bone  
 PT cancer.  
 XX  
 PS Example 15; Page 82; 112pp; English.  
 XX  
 CC The polypeptide sequences represent the 83P5G4-related protein and  
 CC peptide fragments of the protein. 83P5G4 exhibits prostate specific  
 CC expression in normal adult tissue, but it is also aberrantly expressed in  
 CC many cancers including tumours of the prostate, testis, bladder, kidney,  
 CC brain, bone, cervix, uterus, ovary, breast, pancreas, stomach, rectum,  
 CC liver, colon and lung. The 83P5G4 polynucleotide, its related protein and  
 CC peptide fragments and specific PCR primers are therefore useful for  
 CC diagnosing and treating cancer. A vector comprising a polynucleotide  
 CC which encodes a single chain monoclonal antibody, that immunospecifically  
 CC binds to an 83P5G4-related protein, and a ribozyme capable of cleaving a  
 CC polynucleotide having the 83P5G4 coding sequence, are both useful in the  
 CC preparation of a composition for treating a patient with a cancer that  
 CC expresses 83P5G4. The sequences can be used in diagnostic methods to  
 CC monitor the level of 83P5G4 gene products in serum, blood, urine and  
 CC tissue and to thereby detect the presence of cancerous cells  
 XX  
 SQ Sequence 9 AA;

Query Match 83.3%; Score 15; DB 4; Length 9;  
 Best Local Similarity 60.0%; Pred. No. 1.8e+06;  
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KXVXF 5  
 | | |  
 Db 3 KSVAF 7

RESULT 10  
 AAW23266  
 ID AAW23266 standard; peptide; 11 AA.  
 XX  
 AC AAW23266;  
 XX

DT 03-NOV-1997 (first entry)  
 XX  
 DE Tumour necrosis factor alpha inhibiting peptide.  
 XX  
 KW Tumour necrosis factor; alpha; TNF-alpha; inhibition; treatment;  
 KW mediation; disorder; septic shock; bacterium; virus; fungus; infection;  
 KW autoimmune; disease; alcohol induced hepatitis; sarcoiditis; Crohn's;  
 KW disseminated intravascular coagulation; graft versus host; Rawasaki's;  
 KW tumour; bacteria.  
 XX  
 OS Synthetic.  
 XX  
 PN US5641751-A.  
 XX  
 PD 24-JUN-1997.  
 XX  
 PF 01-MAY-1995; 95US-00432694.  
 XX  
 PR 01-MAY-1995; 95US-00432694.  
 XX  
 PA (CENZ ) CENTOCOR INC.  
 XX  
 PI Heavner GA;  
 XX  
 DR WPI; 1997-340972/31.  
 XX  
 PT Peptide inhibiting tumour necrosis factor alpha - useful for treating  
 PT septic shock, infections, autoimmune diseases, etc.  
 XX  
 PS Disclosure; Col 23-24; 15pp; English.  
 XX  
 CC The present peptide is a tumour necrosis factor alpha (TNF-alpha)  
 CC inhibitor, which can be used to treat TNF-alpha mediated disorders, e.g.  
 CC septic shock, bacterial, viral and fungal infections, autoimmune  
 CC diseases, alcohol induced hepatitis, sarcoiditis, Crohn's disease,  
 CC disseminated intravascular coagulation, graft versus host disease,  
 CC Rawasaki's disease and TNF-alpha secreting tumours. The peptide is  
 CC preferably given as a daily dose of 1-1000, preferably 1-10 mg/kg  
 XX  
 SQ Sequence 11 AA;

Query Match 83.3%; Score 15; DB 2; Length 11;  
 Best Local Similarity 60.0%; Pred. No. 3.2e+02;  
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KXVXF 5  
 | | |  
 Db 4 KSVSF 8

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 Job time : 163 secs

OM protein -- protein search, using sw model

Run on: June 29, 2005, 15:40:27 ; Search time 41 Seconds  
(without alignments)  
10.924 Million cell updates/sec

Title: US-10-666-095-7  
Perfect score: 18  
Sequence: 1 KXVFX 6

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 233678

Minimum DB seq length: 0  
Maximum DB seq length: 30

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	15	83.3	11	1	US-08-432-694-16	Sequence 16, Appl
2	15	83.3	14	3	US-09-353-332-3	Sequence 3, Appli
3	15	83.3	15	4	US-09-670-075A-3	Sequence 3, Appli
4	14	77.8	5	2	US-08-612-785B-30	Sequence 30, Appl
5	14	77.8	5	3	US-08-703-675C-43	Sequence 43, Appl
6	14	77.8	5	3	US-08-617-267C-30	Sequence 30, Appl
7	14	77.8	5	3	US-08-617-267C-39	Sequence 39, Appl
8	14	77.8	5	3	US-09-095-106A-40	Sequence 40, Appl
9	14	77.8	5	3	US-09-095-106A-42	Sequence 42, Appl
10	14	77.8	6	4	US-09-747-408-7	Sequence 7, Appli
11	14	77.8	6	4	US-09-747-408-15	Sequence 15, Appl
12	14	77.8	8	1	US-08-457-804-13	Sequence 13, Appl
13	14	77.8	8	3	US-08-444-818-623	Sequence 623, App
14	14	77.8	8	3	US-08-444-818-624	Sequence 624, App
15	14	77.8	8	4	US-08-635-886C-135	Sequence 135, App

16	14	77.8	8	4	US-08-635-886C-136	Sequence 136, App
17	14	77.8	8	4	US-08-974-690C-135	Sequence 135, App
18	14	77.8	8	4	US-08-974-690C-136	Sequence 136, App
19	14	77.8	8	4	US-08-974-685-135	Sequence 135, App
20	14	77.8	8	4	US-08-974-685-136	Sequence 136, App
21	14	77.8	10	2	US-08-537-400-11	Sequence 11, Appl
22	14	77.8	12	1	US-08-305-871A-3	Sequence 3, Appli
23	14	77.8	12	4	US-09-009-953-4	Sequence 4, Appli
24	14	77.8	12	4	US-08-788-822A-4	Sequence 4, Appli
25	14	77.8	12	4	US-09-239-043D-2496	Sequence 2496, Ap
26	14	77.8	14	1	US-08-766-014-21	Sequence 21, Appl
27	14	77.8	14	2	US-08-637-759B-214	Sequence 214, App
28	14	77.8	14	2	US-08-706-702-11	Sequence 11, Appl
29	14	77.8	14	3	US-08-706-706-11	Sequence 11, Appl
30	14	77.8	14	3	US-08-871-355A-214	Sequence 214, App
31	14	77.8	14	3	US-09-019-160-16	Sequence 16, Appl
32	14	77.8	14	3	US-09-201-945-214	Sequence 214, App
33	14	77.8	14	4	US-09-238-471-11	Sequence 11, Appl
34	14	77.8	15	1	US-07-688-748A-1	Sequence 1, Appli
35	14	77.8	15	2	US-08-400-796-14	Sequence 14, Appl
36	14	77.8	18	4	US-09-763-848-4	Sequence 4, Appli
37	14	77.8	22	4	US-09-066-330-4	Sequence 4, Appli
38	14	77.8	23	4	US-09-786-569-13	Sequence 13, Appl
39	14	77.8	23	4	US-09-786-569-14	Sequence 14, Appl
40	14	77.8	23	4	US-09-786-569-16	Sequence 16, Appl
41	14	77.8	23	4	US-09-786-569-17	Sequence 17, Appl
42	14	77.8	23	4	US-09-786-569-18	Sequence 18, Appl
43	14	77.8	23	4	US-09-786-569-19	Sequence 19, Appl
44	14	77.8	23	4	US-09-270-767-57731	Sequence 57731, A
45	14	77.8	24	4	US-09-574-779B-5	Sequence 5, Appli

#### ALIGNMENTS

#### RESULT 1

US-08-432-694-16

; Sequence 16, Application US/08432694

; Patent No. 5641751

; GENERAL INFORMATION:

; APPLICANT: Heavner, George A.

; TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors

; NUMBER OF SEQUENCES: 22

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz &

; ADDRESSEE: No. 5641751ris

; STREET: One Liberty Place, 46th floor

; CITY: Philadelphia

; STATE: PA

; COUNTRY: USA

; ZIP: 19103

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: WordPerfect 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/432,694  
 ; FILING DATE:  
 ; CLASSIFICATION: 514  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: DeLuca, Mark  
 ; REGISTRATION NUMBER: 33,229  
 ; REFERENCE/DOCKET NUMBER: CCOR-0230  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (215) 568-3100  
 ; TELEFAX: (215) 568-3439  
 ; INFORMATION FOR SEQ ID NO: 16:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 11 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: peptide  
 US-08-432-694-16

Query Match 83.3%; Score 15; DB 1; Length 11;  
 Best Local Similarity 60.0%; Pred. No. 98;  
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KXVXF 5  
 | | |  
 Db 4 KSVSF 8

#### RESULT 4

US-08-612-785B-30

; Sequence 30, Application US/08612785B  
 ; Patent No. 5854204

#### GENERAL INFORMATION:

; APPLICANT: Findeis, Mark A. et al.  
 ; TITLE OF INVENTION: Ab Peptides that Modulate b-Amyloid  
 ; TITLE OF INVENTION: Aggregation  
 ; NUMBER OF SEQUENCES: 40  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: LAHIVE & COCKFIELD  
 ; STREET: 28 State Street, Suite 510  
 ; CITY: Boston  
 ; STATE: Massachusetts  
 ; COUNTRY: USA  
 ; ZIP: 02109-1875

#### COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25

#### CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/612,785B  
 ; FILING DATE: Herewith  
 ; CLASSIFICATION: 514

#### PRIOR APPLICATION DATA:

; APPLICATION NUMBER: USSN 08/404,831  
 ; FILING DATE: 14-MAR-1995



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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/475,579
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/548,998
; FILING DATE: 27-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: PPI-002CP3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-612-785B-30

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Query Match          77.8%; Score 14; DB 2; Length 5;
Best Local Similarity 60.0%; Pred. No. 4.1e+05;
Matches      3; Conservative      0; Mismatches      2; Indels      0; Gaps      0;

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Db      1 KLVA F 5

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# RESULT 8

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US-09-095-106A-40
; Sequence 40, Application US/09095106A
; Patent No. 6331440
; GENERAL INFORMATION:
; APPLICANT: NORDSTEDT, Christer
; APPLICANT: NASLUND, Jan
; APPLICANT: THYBERG, Johan
; APPLICANT: TJERNBERG, Lars O.
; APPLICANT: TERENIUS, Lars
; TITLE OF INVENTION: PEPTIDE BINDING THE KLVFF-SEQUENCE OF AMYLOID-BETA
; FILE REFERENCE: 000500-124
; CURRENT APPLICATION NUMBER: US/09/095,106A
; CURRENT FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: US 60/009,386
; PRIOR FILING DATE: 1995-12-29
; PRIOR APPLICATION NUMBER: PCT/SE96/01621
; PRIOR FILING DATE: 1996-12-09
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 40
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Amyloidosis
US-09-095-106A-40

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Best Local Similarity 60.0%; Pred. No. 4.1e+05;  
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 1 KAVFF 5

Search completed: June 29, 2005, 15:55:13  
Job time : 42 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 29, 2005, 15:45:43 ; Search time 156 Seconds  
(without alignments)  
14.790 Million cell updates/sec

Title: US-10-666-095-7  
Perfect score: 18  
Sequence: 1 KXVFX 6

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1717557 seqs, 384547976 residues

Total number of hits satisfying chosen parameters: 384854

Minimum DB seq length: 0  
Maximum DB seq length: 30

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	15	83.3	9	9	US-09-780-053-217	Sequence 217, App
2	15	83.3	9	9	US-09-780-053-326	Sequence 326, App
3	15	83.3	10	9	US-09-780-053-83	Sequence 83, Appl
4	15	83.3	10	9	US-09-780-053-278	Sequence 278, App
5	15	83.3	10	9	US-09-780-053-286	Sequence 286, App
6	15	83.3	10	9	US-09-780-053-300	Sequence 300, App
7	15	83.3	10	9	US-09-780-053-391	Sequence 391, App
8	15	83.3	10	9	US-09-780-053-406	Sequence 406, App
9	15	83.3	10	9	US-09-780-053-709	Sequence 709, App
10	15	83.3	14	13	US-10-016-358-3	Sequence 3, Appli
11	14	77.8	5	9	US-09-850-061A-40	Sequence 40, Appl
12	14	77.8	5	9	US-09-850-061A-42	Sequence 42, Appl
13	14	77.8	5	9	US-09-972-475-30	Sequence 30, Appl
14	14	77.8	5	9	US-09-972-475-39	Sequence 39, Appl
15	14	77.8	5	15	US-10-463-729-30	Sequence 30, Appl
16	14	77.8	5	15	US-10-463-729-39	Sequence 39, Appl
17	14	77.8	5	16	US-10-721-774-40	Sequence 40, Appl
18	14	77.8	5	16	US-10-721-774-42	Sequence 42, Appl
19	14	77.8	6	9	US-09-867-847-16	Sequence 16, Appl
20	14	77.8	6	9	US-09-867-847-24	Sequence 24, Appl
21	14	77.8	6	9	US-09-915-092-6	Sequence 6, Appli
22	14	77.8	6	9	US-09-915-092-14	Sequence 14, Appl
23	14	77.8	6	10	US-09-747-408-7	Sequence 7, Appli
24	14	77.8	6	10	US-09-747-408-15	Sequence 15, Appl
25	14	77.8	6	17	US-10-728-028-6	Sequence 6, Appli
26	14	77.8	6	17	US-10-728-028-14	Sequence 14, Appl
27	14	77.8	6	17	US-10-825-958-14	Sequence 14, Appl
28	14	77.8	6	17	US-10-825-958-22	Sequence 22, Appl
29	14	77.8	8	15	US-10-651-165-135	Sequence 135, App
30	14	77.8	8	15	US-10-651-165-136	Sequence 136, App
31	14	77.8	8	16	US-10-182-040C-21	Sequence 21, Appl
32	14	77.8	8	16	US-10-031-123B-14	Sequence 14, Appl
33	14	77.8	8	17	US-10-808-187-1343	Sequence 1343, Ap
34	14	77.8	9	15	US-10-363-791-208	Sequence 208, App
35	14	77.8	10	10	US-09-572-270A-606	Sequence 606, App
36	14	77.8	10	10	US-09-572-270A-608	Sequence 608, App
37	14	77.8	10	10	US-09-573-822C-646	Sequence 646, App

38	14	77.8	10	15	US-10-363-791-113	Sequence 113, App
39	14	77.8	10	15	US-10-363-791-171	Sequence 171, App
40	14	77.8	10	17	US-10-808-187-551	Sequence 551, App
41	14	77.8	11	17	US-10-808-187-624	Sequence 624, App
42	14	77.8	11	17	US-10-494-175-6	Sequence 6, Appli
43	14	77.8	11	17	US-10-947-352-3	Sequence 3, Appli
44	14	77.8	12	13	US-10-103-395-4	Sequence 4, Appli
45	14	77.8	12	15	US-10-149-138-4208	Sequence 4208, Ap

# ALIGNMENTS

## RESULT 1

US-09-780-053-217

```
; Sequence 217, Application US/09780053
; Patent No. US20020102640A1
; GENERAL INFORMATION:
; APPLICANT: Rene S. Hubert
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Elana Levin
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 83P5G4: A TISSUE SPECIFIC PROTEIN
; TITLE OF INVENTION: HIGHLY EXPRESSED IN PROSTATE CANCER
; FILE REFERENCE: 129.5USU1
; CURRENT APPLICATION NUMBER: US/09/780,053
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,261
; PRIOR FILING DATE: 2000-02-09
; NUMBER OF SEQ ID NOS: 716
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 217
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-780-053-217
```

```
Query Match          83.3%; Score 15; DB 9; Length 9;
Best Local Similarity 60.0%; Pred. No. 1.5e+06;
Matches      3; Conservative      0; Mismatches      2; Indels      0; Gaps      0;
```

```
Qy      1 KXVXF 5
        | | |
Db      3 KSVAF 7
```

Search completed: June 29, 2005, 15:59:03  
Job time : 157 secs

OM protein - protein search, using sw model

Run on: June 29, 2005, 15:32:26 ; Search time 38 Seconds  
(without alignments)  
15.192 Million cell updates/sec

Title: US-10-666-095-7  
Perfect score: 18  
Sequence: 1 KXVXFX 6

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 6283

Minimum DB seq length: 0  
Maximum DB seq length: 30

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_79:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	% Query		Match Length	DB	ID	Description
	Score	Match				
1	14	77.8	17	2	B61491	seed protein ws-2
2	14	77.8	21	2	D61497	seed protein ws-19
3	14	77.8	24	2	PQ0677	photosystem I 9.0K
4	14	77.8	24	2	PQ0676	photosystem I 9.2K
5	14	77.8	24	2	C56819	PS I complex subun
6	14	77.8	26	2	B84724	hypothetical prote
7	14	77.8	29	2	I49732	NADH2 dehydrogenas
8	13	72.2	14	2	S29632	xylan 1,4-beta-xyl
9	13	72.2	16	2	S11805	heat shock protein
10	13	72.2	19	2	A61110	68K collagen-bindi
11	13	72.2	20	2	I49423	cytotoxic T-lympho
12	13	72.2	20	2	S07232	ribulose-bisphosph
13	13	72.2	20	2	PC4385	GroEL protein homo
14	13	72.2	20	2	A44921	hydroxypyruvate re
15	13	72.2	20	2	PC4386	GroEL protein homo

16	13	72.2	20	2	JU0330	hypothetical prote
17	13	72.2	20	2	A61150	2-oxoglutarate dec
18	13	72.2	20	2	A99091	hypothetical prote
19	13	72.2	22	2	A56868	heat shock protein
20	13	72.2	24	2	A40288	chaperonin 60 - Rh
21	13	72.2	28	2	B39116	epidermal growth f
22	13	72.2	30	2	B43591	45K outer membrane
23	13	72.2	30	2	A53415	lectin chain A - I
24	12	66.7	10	2	S48182	bacterioferritin -
25	12	66.7	11	2	PC2372	58K heat shock pro
26	12	66.7	11	2	YHHU	morphogenetic neur
27	12	66.7	11	2	YHBO	morphogenetic neur
28	12	66.7	11	2	YHJFHY	morphogenetic neur
29	12	66.7	11	2	YHXAE	morphogenetic neur
30	12	66.7	11	2	YHRT	morphogenetic neur
31	12	66.7	14	2	S60353	amylopullulanase -
32	12	66.7	14	2	C59137	protein Pf3 - gold
33	12	66.7	16	2	S22677	heat shock protein
34	12	66.7	16	2	S24667	protein-tyrosine k
35	12	66.7	17	2	S05930	chorion class B pr
36	12	66.7	17	2	S05922	chorion class B pr
37	12	66.7	17	2	S05936	chorion class B pr
38	12	66.7	20	2	C60894	gamma crystallin I
39	12	66.7	21	2	A36902	orfB2 - Escherichi
40	12	66.7	26	2	S26228	ribosomal protein
41	12	66.7	30	2	S15678	acetylcholinestera
42	12	66.7	30	2	B29164	cartilage proteogl
43	12	66.7	30	2	B81956	hypothetical prote
44	12	66.7	30	2	D82251	hypothetical prote
45	11	61.1	9	2	B20569	serum amyloid P-co

# ALIGNMENTS

## RESULT 1

B61491

seed protein ws-2 - winged bean (fragment)

C;Species: Psophocarpus tetragonolobus (winged bean)

C;Date: 07-Oct-1994 #sequence\_revision 07-Oct-1994 #text\_change 09-Jul-2004

C;Accession: B61491

R;Hirano, H.

J. Protein Chem. 8, 115-130, 1989

A;Title: Microsequence analysis of winged bean seed proteins electroblotted from two-dimensional gel.

A;Reference number: A61491; MUID:89351606; PMID:2765119

A;Accession: B61491

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-17 <HIR>

A;Cross-references: UNIPROT:Q7M1H7

C;Keywords: seed

Query Match 77.8%; Score 14; DB 2; Length 17;

Best Local Similarity 40.0%; Pred. No. 2.1e+02;

Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

$$| : |$$

Job time : 40 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: June 29, 2005, 15:24:30 ; Search time 165 Seconds

(without alignments)

18.621 Million cell updates/sec

Title: US-10-666-095-7

Perfect score: 18

Sequence: 1 KXVFX 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 26236

Minimum DB seq length: 0

Maximum DB seq length: 30

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 03:\*

```
1:  uniprot  sprout:*
```

```
2: uniprot trembl:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	15	83.3	20	2	Q9R497	Q9r497 vibrio chol
2	14	77.8	8	2	Q56759	Q56759 xanthobacte
3	14	77.8	14	2	Q85718	Q85718 reovirus ty
4	14	77.8	17	2	Q7M1H7	Q7mlh7 psophocarpu
5	14	77.8	19	2	Q85671	Q85671 reovirus ty
6	14	77.8	20	2	Q85670	Q85670 reovirus ty
7	14	77.8	21	2	Q7M1H8	Q7mlh8 psophocarpu
8	14	77.8	23	1	CH60 THIFE	P29134 thiobacillu

9	14	77.8	24	1	PSAH_CU CSA	P42050	cucumis sat
10	14	77.8	24	2	Q714T9	Q714t9	fragilaria
11	14	77.8	24	2	Q9T2J0	Q9t2j0	nicotiana t
12	14	77.8	24	2	Q9T2J1	Q9t2j1	nicotiana t
13	14	77.8	25	2	Q72001	Q72001	human immun
14	14	77.8	29	1	NUO1_SOLTU	P80267	solanum tub
15	14	77.8	30	2	Q8CTE8	Q8cte8	staphylococ
16	13	72.2	8	2	Q93SP2	Q93sp2	pseudomonas
17	13	72.2	13	1	CH60_CANFA	P49818	canis famil
18	13	72.2	14	2	Q9UH91	Q9uh91	homo sapien
19	13	72.2	14	2	Q7M0Q6	Q7m0q6	thermotoga
20	13	72.2	17	2	Q9S889	Q9s889	narcissus p
21	13	72.2	18	1	RL24_PROVU	P20032	proteus vul
22	13	72.2	18	1	RL24_SERMA	P49624	serratia ma
23	13	72.2	18	2	Q9R522	Q9r522	francisella
24	13	72.2	20	2	Q7RR59	Q7rr59	plasmodium
25	13	72.2	20	2	Q7M266	Q7m266	euglena gra
26	13	72.2	20	2	Q9S8P0	Q9s8p0	raphanus sa
27	13	72.2	20	2	Q49132	Q49132	methylobact
28	13	72.2	20	2	Q8CYA3	Q8cya3	streptococc
29	13	72.2	20	2	Q62546	Q62546	mus spretus
30	13	72.2	21	2	P70861	P70861	borrelia bu
31	13	72.2	22	1	CH60_BOVIN	P31081	bos taurus
32	13	72.2	22	2	Q9TLD2	Q9tld2	bostrychia
33	13	72.2	23	2	Q8MFI5	Q8mfi5	sphaerocion
34	13	72.2	23	2	Q8MFI9	Q8mfi9	hymenophyll
35	13	72.2	23	2	Q8MFJ1	Q8mfj1	hymenophyll
36	13	72.2	23	2	Q8MFJ3	Q8mfj3	hymenophyll
37	13	72.2	23	2	Q8MFJ5	Q8mfj5	hymenophyll
38	13	72.2	23	2	Q8MFJ7	Q8mfj7	hymenophyll
39	13	72.2	23	2	Q8MFJ9	Q8mfj9	hymenophyll
40	13	72.2	23	2	Q8MFK1	Q8mfk1	hymenophyll
41	13	72.2	23	2	Q8MFK3	Q8mfk3	hymenophyll
42	13	72.2	23	2	Q8MFK5	Q8mfk5	hymenophyll
43	13	72.2	23	2	Q9R590	Q9r590	neisseria m
44	13	72.2	24	1	CH60_ACICA	P81874	acinetobact
45	13	72.2	24	1	CH60_HELVI	P26317	heliothis v

# ALIGNMENTS

## RESULT 1

Q9R497

ID Q9R497 PRELIMINARY; PRT; 20 AA.

AC Q9R497;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)

DE Outer membrane protein 38 kDa monomeric subunit (Fragment).

OS Vibrio cholerae.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;

OC Vibrionaceae; Vibrio.

OX NCBI\_TaxID=666;

RN [1]

RP SEQUENCE.

RX MEDLINE=96134988; PubMed=8550475;



RA Chakrabarti S.R., Chaudhuri K., Sen K., Das J.;  
RT "Porins of Vibrio cholerae: purification and characterization of  
RT OmpU.";  
RL J. Bacteriol. 178:524-530(1996).  
SQ SEQUENCE 20 AA; 2199 MW; CF50A18B305A5052 CRC64;

Query Match 83.3%; Score 15; DB 2; Length 20;  
Best Local Similarity 60.0%; Pred. No. 6.8e+02;  
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KXVXF 5  
| | |  
Db 9 KAVSF 13

Search completed: June 29, 2005, 15:45:34  
Job time : 168 secs